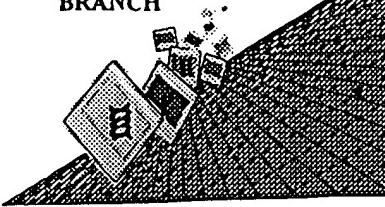


RAW SEQUENCE LISTING ERROR REPORT



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 19/920262

Source: CIP E

Date Processed by STIC: 08/09/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>09/920,262</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input checked="" type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

Does Not Comply
Corrected Diskette Needed

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/920,262

DATE: 08/09/2001
TIME: 14:31:25

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\08092001\I920262.raw

4 <110> APPLICANT: Shealy, David; Knight, David; Scallon, Bernie; Giles-Komar, Jill;
Peritt,
5 David
7 <120> TITLE OF INVENTION: IL-12 ANTIBODIES, COMPOSITIONS, METHODS AND USES
9 <130> FILE REFERENCE: CEN248
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/920,262
C--> 11 <141> CURRENT FILING DATE: 2001-08-01
11 <160> NUMBER OF SEQ ID NOS: 15
13 <170> SOFTWARE: PatentIn Ver 2.0

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

ERRORED SEQUENCES

Errored

15 <210> SEQ ID NO: 1
16 <211> LENGTH: 5
17 <212> TYPE: PRT
18 <213> ORGANISM: Homo sapiens
W--> 19 <400> SEQUENCE: 1
21 Thr Tyr Trp Leu Gly *see item 3 on Error Summary Sheet*
E--> 22 1 5
56 <210> SEQ ID NO: 5
57 <211> LENGTH: 7
58 <212> TYPE: PRT
59 <213> ORGANISM: Homo sapiens
W--> 60 <400> SEQUENCE: 5
62 Ala Ala Ser Ser Leu Gln Ser
E--> 63 1 5 5 *see item 3*
233 <210> SEQ ID NO: 10
234 <211> LENGTH: 15
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
W--> 237 <400> SEQUENCE: 10
E--> 238 agatatacta-tgcac *15* *Errored: Sequence 13*
239 15
255 <210> SEQ ID NO: 13
256 <211> LENGTH: 33
257 <212> TYPE: DNA
258 <213> ORGANISM: Homo sapiens
W--> 259 <400> SEQUENCE: 13
E--> 260 ctctcctgca gggcagtc gagtgttagc agtacttttag cc *33*

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

33 nucleotides indicated
42 nucleotides found

262 <210> SEQ ID NO: 14
263 <211> LENGTH: 21 *18*
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
W--> 266 <400> SEQUENCE: 14
E--> 267 gatgcattca acaggccc
269 <210> SEQ ID NO: 15
270 <211> LENGTH: 27 *27* *27 nucleotides indicated*
21 nucleotides found

18

18

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/920,262

DATE: 08/09/2001
TIME: 14:31:25

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\08092001\I920262.raw

271 <212> TYPE: DNA
272 <213> ORGANISM: Homo sapiens
W--> 273 <400> SEQUENCE: 15
274 cagcagcgta gcaactggcc t
E--> 278 cEn 248 4
E--> 280 1
E--> 283 4

21 nucleotides found

21

delete

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/920,262

DATE: 08/09/2001
TIME: 14:31:26

Input Set : A:\PTO_VSK.txt
Output Set: N:\CRF3\08092001\I920262.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:19 M:283 W: Missing Blank Line separator, <400> field identifier
L:22 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:30 M:283 W: Missing Blank Line separator, <400> field identifier
L:42 M:283 W: Missing Blank Line separator, <400> field identifier
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:60 M:283 W: Missing Blank Line separator, <400> field identifier
L:63 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:69 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:283 W: Missing Blank Line separator, <400> field identifier
L:108 M:283 W: Missing Blank Line separator, <400> field identifier
L:135 M:283 W: Missing Blank Line separator, <400> field identifier
L:237 M:283 W: Missing Blank Line separator, <400> field identifier
L:238 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:10
L:245 M:283 W: Missing Blank Line separator, <400> field identifier
L:252 M:283 W: Missing Blank Line separator, <400> field identifier
L:259 M:283 W: Missing Blank Line separator, <400> field identifier
L:260 M:254 E: No. of Bases conflict, LENGTH:Input:33 Counted:42 SEQ:13
L:260 M:252 E: No. of Seq. differs, <211>LENGTH:Input:33 Found:42 SEQ:13
L:266 M:283 W: Missing Blank Line separator, <400> field identifier
L:267 M:252 E: No. of Seq. differs, <211>LENGTH:Input:21 Found:18 SEQ:14
L:273 M:283 W: Missing Blank Line separator, <400> field identifier
L:278 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:278 M:254 E: No. of Bases conflict, LENGTH:Input:4 Counted:24 SEQ:15
L:278 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1
L:278 M:112 C: (48) String data converted to lower case,
M:254 Repeated in SeqNo=15
L:283 M:252 E: No. of Seq. differs, <211>LENGTH:Input:27 Found:24 SEQ:15